

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Wahl, Geoffrey M  
O'Gorman, Stephen V
- (ii) TITLE OF INVENTION: FLP-MEDIATED GENE MODIFICATION IN  
MAMMALIAN CELLS, AND COMPOSITIONS AND CELLS USEFUL  
THEREFOR
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
  - (B) STREET: 444 South Flower Street, Suite 2000
  - (C) CITY: Los Angeles
  - (D) STATE: California
  - (E) COUNTRY: USA
  - (F) ZIP: 90071
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/484,324
  - (B) FILING DATE: 07-JUN-1995
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Reiter, Stephen E
  - (B) REGISTRATION NUMBER: 31,192
  - (C) REFERENCE/DOCKET NUMBER: P41 9984
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (619) 546-4737
  - (B) TELEFAX: (619) 546-9392

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1380 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: NATIVE FLP
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..1269
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG CCA CAA TTT GAT ATA TTA TGT AAA ACA CCA CCT AAG GTG CTT GTT  
 Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu Val  
 1 5 10 15

CGT Arg	CAG Gln	TTT Phe	GTG Val 20	GAA Glu	AGG Arg	TTT Phe	GAA Glu	AGA Arg 25	CCT Pro	TCA Ser	GGT Gly	GAG Glu	AAA Lys 30	ATA Ile	GCA Ala	96
TTA Leu	TGT Cys	GCT Ala 35	GCT Ala	GAA Glu	CTA Leu	ACC Thr	TAT Tyr 40	TTA Leu	TGT Cys	TGG Trp	ATG Met	ATT Ile 45	ACA Thr	CAT His	AAC Asn	144
GGA Gly	ACA Thr 50	GCA Ala	ATC Ile	AAG Lys	AGA Arg	GCC Ala 55	ACA Thr	TTC Phe	ATG Met	AGC Ser	TAT Tyr 60	AAT Asn	ACT Thr	ATC Ile	ATA Ile	192
AGC Ser 65	AAT Asn	TCG Ser	CTG Leu	AGT Ser	TTC Phe 70	GAT Asp	ATT Ile	GTC Val	AAT Asn	AAA Lys 75	TCA Ser	CTC Leu	CAG Gln	TTT Phe	AAA Lys 80	240
TAC Tyr	AAG Lys	ACG Thr	CAA Gln	AAA Lys 85	GCA Ala	ACA Thr	ATT Ile	CTG Leu 90	GAA Glu	GCC Ala	TCA Ser	TTA Leu	AAG Lys 95	AAA Lys 95	TTG Leu	288
ATT Ile	CCT Pro	GCT Ala 100	TGG Trp	GAA Glu	TTT Phe	ACA Thr	ATT Ile 105	ATT Ile 105	CCT Pro	TAC Tyr	TAT Tyr	GGA Gly 110	CAA Gln 110	AAA Lys	CAT His	336
CAA Gln	TCT Ser	GAT Asp 115	ATC Ile	ACT Thr	GAT Asp	ATT Ile	GTA Val 120	AGT Ser	AGT Ser	TTG Leu	CAA Gln 125	TTA Leu 125	CAG Gln	TTC Phe	GAA Glu	384
TCA Ser	TCG Ser 130	GAA Glu	GAA Glu	GCA Ala	GAT Asp	AAG Lys 135	GGA Gly	AAT Asn	AGC Ser	CAC His	AGT Ser 140	AAA Lys	AAA Lys	ATG Met	CTT Leu	432
AAA Lys 145	GCA Ala	CTT Leu	CTA Leu	AGT Ser	GAG Glu 150	GGT Gly	GAA Glu	AGC Ser	ATC Ile	TGG Trp 155	GAG Glu	ATC Ile	ACT Thr	GAG Glu	AAA Lys 160	480
ATA Ile	CTA Leu	AAT Asn	TCG Ser	TTT Phe 165	GAG Glu	TAT Tyr	ACT Thr	TCG Ser 170	AGA Arg	TTT Phe	ACA Thr	AAA Lys	ACA Thr	AAA Lys 175	ACT Thr	528
TTA Leu	TAC Tyr	CAA Gln 180	TTC Phe	CTC Leu	TTC Phe	CTA Leu	GCT Ala 185	ACT Thr	TTC Phe	ATC Ile	AAT Asn	TGT Cys 190	GGA Gly 190	AGA Arg	TTC Phe	576
AGC Ser	GAT Asp	ATT Ile 195	AAG Lys	AAC Asn	GTT Val	GAT Asp	CCG Pro 200	AAA Lys	TCA Ser	TTT Phe	AAA Lys	TTA Leu 205	GTC Val	CAA Gln	AAT Asn	624
AAG Lys	TAT Tyr 210	CTG Leu	GGA Gly	GTA Val	ATA Ile	ATC Ile 215	CAG Gln	TGT Cys	TTA Leu	GTG Val	ACA Thr 220	GAG Glu	ACA Thr	AAG Lys	ACA Thr	672
AGC Ser 225	GTT Val	AGT Ser	AGG Arg	CAC His	ATA Ile 230	TAC Tyr	TTC Phe	TTT Phe	AGC Ser	GCA Ala 235	AGG Arg	GGT Gly	AGG Arg	ATC Ile	GAT Asp 240	720
CCA Pro	CTT Leu	GTA Val	TAT Tyr	TTG Leu 245	GAT Asp	GAA Glu	TTT Phe	TTG Leu 250	AGG Arg	AAT Asn	TCT Ser	GAA Glu	CCA Pro 255	GTC Val	CTA Leu	768
AAA Lys	CGA Arg	GTA Val 260	AAT Asn	AGG Arg	ACC Thr	GGC Gly	AAT Asn 265	TCT Ser 265	TCA Ser	AGC Ser	AAT Asn	AAA Lys 270	CAG Gln 270	GAA Glu	TAC Tyr	816
CAA Gln	TTA Leu 275	TTA Leu	AAA Lys	GAT Asp	AAC Asn	TTA Leu 280	GTC Val 280	AGA Arg	TCG Ser	TAC Tyr	AAT Asn	AAA Lys 285	GCT Ala 285	TTG Leu	AAG Lys	864

AAA AAT GCG CCT TAT TCA ATC TTT GCT ATA AAA AAT GGC CCA AAA TCT	912
Lys Asn Ala Pro Tyr Ser Ile Phe Ala Ile Lys Asn Gly Pro Lys Ser	
290 295 300	
CAC ATT GGA AGA CAT TTG ATG ACC TCA TTT CTT TCA ATG AAG GGC CTA	960
His Ile Gly Arg His Leu Met Thr Ser Phe Leu Ser Met Lys Gly Leu	
305 310 315 320	
ACG GAG TTG ACT AAT GTT GTG GGA AAT TGG AGC GAT AAG CGT GCT TCT	1008
Thr Glu Leu Thr Asn Val Val Gly Asn Trp Ser Asp Lys Arg Ala Ser	
325 330 335	
GCC GTG GCC AGG ACA ACG TAT ACT CAT CAG ATA ACA GCA ATA CCT GAT	1056
Ala Val Ala Arg Thr Thr Tyr Thr His Gln Ile Thr Ala Ile Pro Asp	
340 345 350	
CAC TAC TTC GCA CTA GTT TCT CGG TAC TAT GCA TAT GAT CCA ATA TCA	1104
His Tyr Phe Ala Leu Val Ser Arg Tyr Tyr Ala Tyr Asp Pro Ile Ser	
355 360 365	
AAG GAA ATG ATA GCA TTG AAG GAT GAG ACT AAT CCA ATT GAG GAG TGG	1152
Lys Glu Met Ile Ala Leu Lys Asp Glu Thr Asn Pro Ile Glu Glu Trp	
370 375 380	
CAG CAT ATA GAA CAG CTA AAG GGT AGT GCT GAA GGA AGC ATA CGA TAC	1200
Gln His Ile Glu Gln Leu Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr	
385 390 395 400	
CCC GCA TGG ATT GGG ATA ATA TCA CAG GAG GTA CTA GAC TAC CTT TCA	1248
Pro Ala Trp Ile Gly Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Ser	
405 410 415	
TCC TAC ATA AAT AGA CGC ATA TAAGTACGCA TTAAAGCATA AACACGCACT	1299
Ser Tyr Ile Asn Arg Arg Ile	
420	
ATCCCGTTCT TCTCATGTAT ATATATATAC AGGCAACACG CAGATATAGG TGCGACGTGA	1359
ACAGTGAGCT GTATGTGCGC A	1380

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu Val	
1 5 10 15	
Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys Ile Ala	
20 25 30	
Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile Thr His Asn	
35 40 45	
Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr Ile Ile	
50 55 60	
Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gln Phe Lys	
65 70 75 80	

Tyr Lys Thr Gln Lys<sub>85</sub> Ala Thr Ile Leu Glu<sub>90</sub> Ala Ser Leu Lys<sub>95</sub> Lys Leu  
 Ile Pro Ala Trp<sub>100</sub> Glu Phe Thr Ile Ile<sub>105</sub> Pro Tyr Tyr Gly Gln<sub>110</sub> Lys His  
 Gln Ser Asp<sub>115</sub> Ile Thr Asp Ile<sub>120</sub> Val Ser Ser Leu Gln<sub>125</sub> Leu Gln Phe Glu  
 Ser Ser<sub>130</sub> Glu Glu Ala Asp Lys<sub>135</sub> Gly Asn Ser His Ser<sub>140</sub> Lys Lys Met Leu  
 Lys<sub>145</sub> Ala Leu Leu Ser Glu<sub>150</sub> Gly Glu Ser Ile Trp<sub>155</sub> Glu Ile Thr Glu Lys<sub>160</sub>  
 Ile Leu Asn Ser<sub>165</sub> Phe Glu Tyr Thr Ser Arg<sub>170</sub> Phe Thr Lys Thr<sub>175</sub> Lys Thr  
 Leu Tyr Gln Phe<sub>180</sub> Leu Phe Leu Ala Thr<sub>185</sub> Phe Ile Asn Cys Gly<sub>190</sub> Arg Phe  
 Ser Asp Ile<sub>195</sub> Lys Asn Val Asp<sub>200</sub> Pro Lys Ser Phe Lys Leu<sub>205</sub> Val Gln Asn  
 Lys Tyr Leu Gly Val Ile<sub>215</sub> Ile Gln Cys Leu Val Thr<sub>220</sub> Glu Thr Lys Thr  
 Ser<sub>225</sub> Val Ser Arg His<sub>230</sub> Ile Tyr Phe Phe Ser Ala<sub>235</sub> Arg Gly Arg Ile Asp<sub>240</sub>  
 Pro Leu Val Tyr<sub>245</sub> Leu Asp Glu Phe Leu Arg<sub>250</sub> Asn Ser Ser Glu Pro Val<sub>255</sub> Leu  
 Lys Arg Val<sub>260</sub> Asn Arg Thr Gly Asn<sub>265</sub> Ser Ser Ser Asn Lys<sub>270</sub> Gln Glu Tyr  
 Gln Leu Leu<sub>275</sub> Lys Asp Asn Leu Val Arg Ser Tyr Asn Lys<sub>285</sub> Ala Leu Lys  
 Lys Asn Ala Pro Tyr Ser Ile<sub>295</sub> Phe Ala Ile Lys Asn Gly Pro Lys Ser  
 His<sub>305</sub> Ile Gly Arg His<sub>310</sub> Leu Met Thr Ser Phe Leu Ser Met Lys Gly Leu<sub>320</sub>  
 Thr Glu Leu Thr Asn<sub>325</sub> Val Val Gly Asn Trp<sub>330</sub> Ser Asp Lys Arg Ala Ser<sub>335</sub>  
 Ala Val Ala Arg<sub>340</sub> Thr Thr Tyr Thr His Gln Ile Thr Ala Ile Pro Asp  
 His Tyr Phe<sub>355</sub> Ala Leu Val Ser Arg<sub>360</sub> Tyr Tyr Ala Tyr Asp<sub>365</sub> Pro Ile Ser  
 Lys Glu Met Ile Ala Leu Lys<sub>375</sub> Asp Glu Thr Asn Pro<sub>380</sub> Ile Glu Glu Trp  
 Gln His Ile Glu Gln Leu Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr  
 385 390 395 400  
 Pro Ala Trp Ile Gly<sub>405</sub> Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Ser  
 410 415  
 Ser Tyr Ile Asn Arg Arg Ile  
 420

330 340 350 360 370 380 390 400 410 420

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAAGTTCCTA TTCTCTAGAA AGTATAGGAA CTTC

34

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 68 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GATCCCGGGC TACCATGGAG AAGTTCCTAT TCCGAAGTTC CTATTCTCTA GAAAGTATAG

60

GAACTTCA

68

"1993-1994" 1993-1994